

AMENDMENTS TO THE CLAIMS

1. (Canceled)
2. (Canceled)
3. (Canceled)
4. (Canceled)
5. (Canceled)
6. (Canceled)
7. (Canceled)
8. (Canceled)
9. (Canceled)
10. (Canceled)
11. (Canceled)
12. (Currently Amended) A method for inferring genomic sequences unique to at least one set of organisms other than a set of organisms under investigation, the method comprising:
 - obtaining genomic data characteristic of a set of organisms under investigation;
 - formatting the genomic data into at least one query-length sequence, each query-length sequence being of a format compatible with a similarity search engine;
 - searching a selected genomic database using the query-length sequence and the similarity search engine,
 - the selected genomic database containing genomic data from a plurality of organisms;

parsing ~~the results of the search for those sequences having homology above a threshold with at least one set of organisms other than the set under investigation and otherwise unique within the selected genomic database.~~
outputting to ~~memory a user~~ an identity of those sequences having homology above a threshold with at least one set of organisms other than the set under investigation and otherwise unique within the selected genomic database.

13. (Currently amended) A computer program product for inferring genomic sequences unique to a at least one set of organisms other than a set of organisms under investigation, the computer program product comprising:

- a computer-readable physical medium;
- a genomic data interface module, stored on the medium and operable to couple to a source of genomic data to receive genomic data characteristic of a set of organisms under investigation;
- a formatting module, stored on the medium and operable to format received genomic data into at least one query-length sequence, each query-length sequence being of a format compatible with a similarity search engine;
- a search interface module, stored on the medium and operable to interface with the similarity search engine to submit the query-length sequence to a selected genomic database containing genomic data from a substantial plurality of organisms ; and
- a search results parsing module, stored on the medium and operable to parse ~~the results of the search for those sequences having homology above a threshold with at least one set of organisms other than the set under investigation and otherwise unique within the selected genomic database.~~ and to output to ~~memory a user~~ an identity of those sequences having homology above a threshold with at least one set of organisms other than the set under investigation and otherwise unique within the selected genomic database.

14. (New) A method for inferring genomic sequences unique to a first set of organisms, the method comprising:

obtaining genomic data characteristic of a second set of organisms;

formatting the second set genomic data into at least one query-length sequence, each query-length sequence being of a format compatible with a similarity search engine;

searching a selected genomic database using the query-length sequence and the similarity search engine, the selected genomic database containing genomic data from a plurality of organisms including the first set of organisms;

parsing results of the search for those sequences, other than sequences of the second set, having homology above a threshold with the second set and otherwise unique within the selected genomic database,

outputting to a user an identity of those sequences having homology above a threshold with the second set and otherwise unique within the selected genomic database as genomic sequences unique to the first set.